

Serum Protein Triplet TGF- β 1, TIMP-1, and YKL-40 Serve as Diagnostic and Prognostic Profile for Astrocytoma

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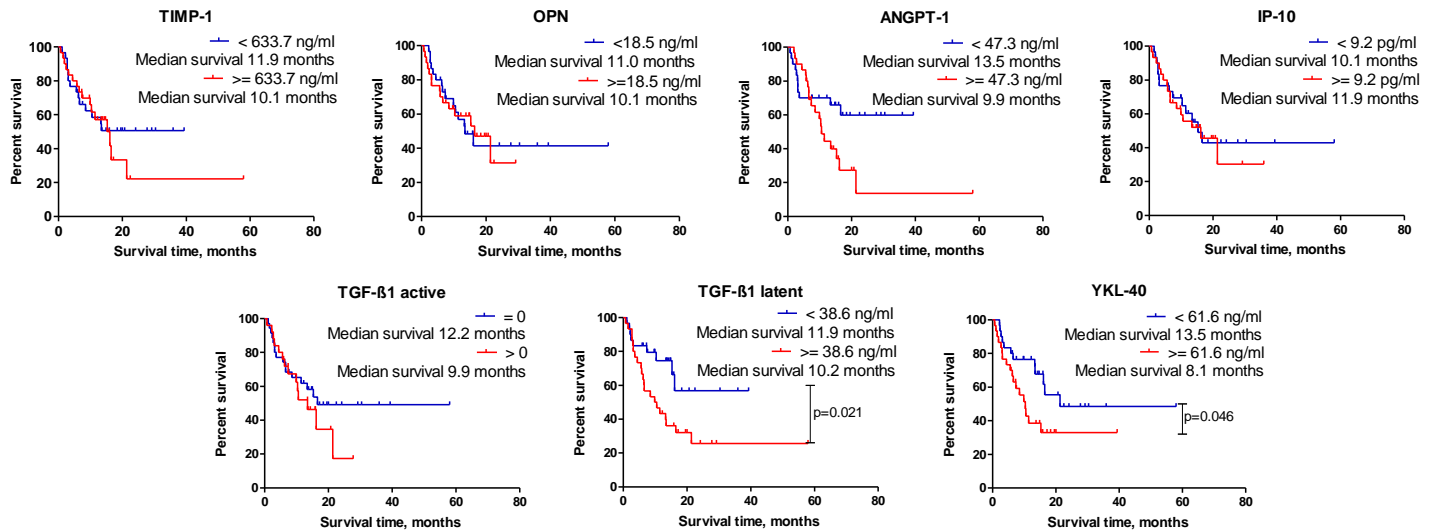


Figure S1. Survival dependency on TIMP-1, OPN, ANGPT-1, IP-10, active and latent TGF-β1, and YKL-40 proteins concentration in glioblastoma patients peripheral blood serum. TIMP-1 ($n = 60$), low (< 633.7 ng/mL) vs. high (≥ 633.7 ng/mL) protein level patient group with median survival of 11.9 months versus 10.1 months, respectively; log-rank test; $\chi^2 = 0.306$; $df = 1$; $p = 0.580$; OPN ($n = 60$), low (< 18.5 ng/mL) vs. high (≥ 18.5 ng/mL) protein level patient group with median survival of 11.0 months versus 10.1 months, respectively; log-rank test; $\chi^2 = 0.015$; $df = 1$; $p = 0.902$; ANGPT-1 ($n = 60$), low (< 47.3 ng/mL) vs. high (≥ 47.3 ng/mL) protein level patient group with median survival of 13.5 months versus 9.9 months, respectively; log-rank test; $\chi^2 = 3.502$; $df = 1$; $p = 0.061$; IP-10 ($n = 60$), low (< 9.2 pg/mL) vs. high (≥ 9.2 pg/mL) protein level patient group with median survival of 10.1 months versus 11.9 months, respectively; log-rank test; $\chi^2 = 0.102$; $df = 1$; $p = 0.749$; active TGF-β1 ($n = 60$), low (0 pg/mL) vs. high (> 0 pg/mL) protein level patient group with median survival of 12.2 months versus 9.9 months, respectively; log-rank test; $\chi^2 = 0.843$; $df = 1$; $p = 0.359$; latent TGF-β1 ($n = 60$), low (< 38.6 ng/mL) vs. high (≥ 38.6 ng/mL) protein level patient group with median survival of 11.9 months versus 10.2 months, respectively; log-rank test; $\chi^2 = 5.308$; $df = 1$; $p = 0.021$; YKL-40 ($n = 60$), low (< 61.6 ng/mL) vs. high (≥ 61.6 ng/mL) protein level patient group with median survival of 13.5 months versus 8.1 months, respectively; log-rank test; $\chi^2 = 3.967$; $df = 1$; $p = 0.046$; Blue colour – low protein level, red colour – high protein level.

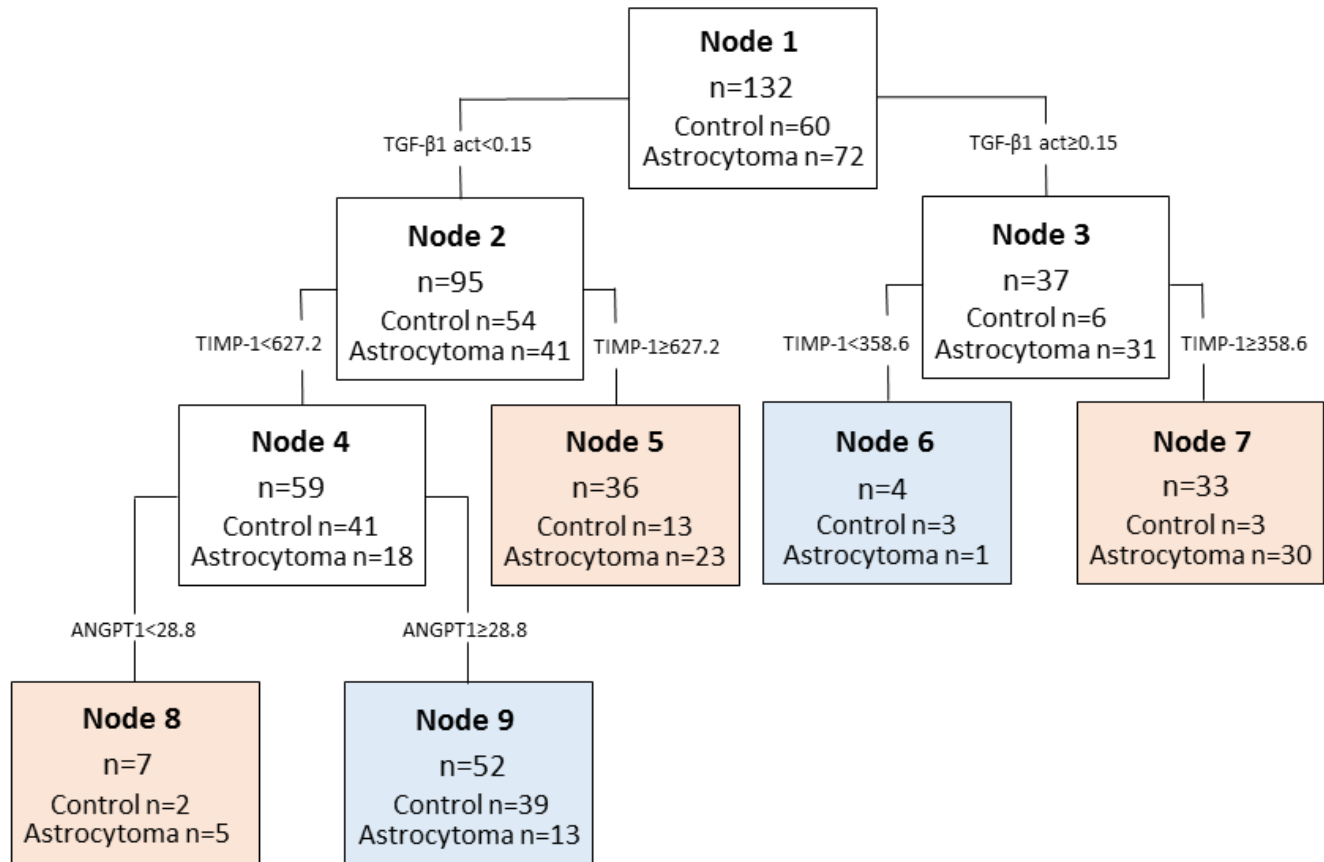


Figure S2. Astrocytoma detection tree model, composed of active (act) TGF-β1, TIMP-1 and ANGPT-1 proteins in astrocytoma and healthy control serum. Tree was calculated from the result of 132 participants (60 – controls and 72 - astrocytomas). The number of all participants assigned to the specific class is represented by n, below – the number of participants in healthy control and astrocytoma group. Rose colour nodes represent classes, which predict participant having astrocytoma, blue nodes – healthy participant.